

REMARKS

Claims 1-10 12-17, 27 and 30 have been cancelled, without prejudice or disclaimer.

Claim 11 has been amended to recite a sequence identity of 80% identity in order to facilitate prosecution.

Support for the amendment can be found at least on page 9, lines 12-14 of the instant specification. No new matter has been added.

Claim numbers 25, 26 and 27 were changed back to original claim numbers (i.e., 26, 28 and 29), since the previous amendment of the claim numbers was improper. Thus, claims 11-24, 26, 28 and 29 are currently pending. Claims 11-19, 23, 24, 26, 28 and 29 stand rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Specifically, it is stated in the Office Action that while the specification indicates alterations in nucleotide sequence such as alterations that produce a chemically equivalent amino acid at a given site or alterations in the N- or C-terminal portions that are not expected to alter functionality, it does not provide the sites of alteration in the nucleotide sequence, nor identify the resulting sequence encoding a functional enzyme.

Furthermore, the two motifs of Choe et al. that are found in the claimed sequence, are not described in the specification and the specification does not indicate the claimed variants of SEQ ID NO:2 that are required to contain these motifs. Consequently, there does not appear to be a correlation of structure and function with respect to the peptide variants encoded by the polynucleotides.

Submitted herewith in Appendix A is an alignment of SEQ ID NO:2 of the pending claims with the pepper cytochrome P450 polypeptide sequence (Table 3 & 4 of instant application; NCBI GI No. 6739506). A similar alignment was submitted previously, but the alignment now also indicates conservative amino acid changes by an arrowhead on the top row. Amino acids conserved among all sequences are indicated with an asterisk (*) above the alignment; dashes are used by the program to maximize alignment of the sequences.

The two motifs of Choe et al. (The Plant Cell (1998) 10: 231-243, submitted previously) appear underlined in the alignment. These motifs are typical of cytochrome P450 enzymes and include the consensus sequence (A/G)GX(D/E)T(T/S) and a heme-binding domain with the consensus sequence PFG(A/S/V)GRRXC(P/A/V)G and can be found in the sequence of the instant invention.

One skilled in the art would appreciate that the more highly conserved a residue is, the less likely that it could be modified and function maintained. From this alignment and the domains illustrated in the attached Appendix, one could quickly determine which amino acid residues might be modified in SEQ ID NO:2 without a likely change in function.

Since the protein from pepper and SEQ ID NO:2 share only about 40.4% sequence identity, one of skill in the art would appreciate that many variants sharing at least 80% identity to SEQ ID NO:2 would retain the claimed activity. In addition, the specification on page 7, line 4 through page 8 line 11, teaches technical considerations for the substitution of amino acids in ways that do not change functionality.

Principally, certain alterations in the nucleic acid fragment can encode substitute amino acids that have similar charge and/or hydrophobicity (e.g. the conservative amino acid changes indicated in the alignment by an arrowhead) or results in N-terminal or C-terminal variation of the peptide which do not affect functionality. The specification further discloses that the practice of amino acid substitution to retain biological activity is well within the routine skill in the art. With this information, a skilled artisan could review the characterized sequences and identify a variety of sequences sharing at least 80% identity to SEQ ID NO:2.

The law is well settled that what is conventional or well known to one of ordinary skill in the art need not be disclosed in detail. See *Hybritech Inc. v. Monoclonal Antibodies, Inc.* 231 USPQ 81, 94 (Fed. Cir. 1986).

It is respectfully submitted that the claimed invention is described in the specification in such a way as to reasonably convey to one skilled in the relevant art, at the time the application was filed, that Applicants were in possession of the invention as recited in Claims 11-19, 23, 24, 26, 28 and 29.

In view of above discussion, it is respectfully submitted that sufficient relevant identifying characteristics have been disclosed to allow one skilled in the art to predictably determine mutants, allelic variants and cytochrome P450 enzymes capable of producing delta12-epoxygenated fatty acids from other plants and organisms.

Accordingly, withdrawal of the rejection of claims 11-19, 23, 24, 26, 28 and 29 under 35 USC §112, first paragraph, is respectfully requested.

It is believed that the claims are now in form for allowance which allowance is respectfully solicited.

A petition for a one (1) month extension of time and a Notice of Appeal accompany this Response After Final along with a copy of Appendix A.

Please charge any fees or credit any overpayment of fees, which are required in connection herewith to Deposit Account No. 04-1928 (E.I. duPont de Nemours and Company).

Respectfully submitted,

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Dated: August 15, 2007